

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:59 ; Search time 32.09 Seconds
(without alignments)
303.844 Million cell updates/sec

Title: US-09-772-103-8
Perfect score: 655
Sequence: I MDFQVQIFSFLLISASVILS.....CQWSSVPLTFGGTKVEIK 128
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
al number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	76.6	130	2 A32513	Ig kappa chain pre
2	499	76.2	130	1 JLO079	Ig kappa chain pre
3	498	76.0	235	2 S25058	Ig kappa chain - m
4	491	75.0	140	2 PL0013	Ig kappa chain pre
5	478	73.0	130	2 S04573	Ig kappa chain pre
6	466	71.1	130	2 B32456	Ig kappa chain pre
7	463.5	70.8	107	2 S36264	Ig lambda chain v
8	463.5	70.8	108	2 B49047	Ig kappa chain v r
9	463.5	70.8	125	2 S40349	Ig kappa chain v-j
10	455.5	69.5	129	2 S2793	Ig kappa chain v r
11	454.5	69.4	107	2 S36269	Ig lambda chain v
12	454.5	69.4	129	2 S40317	Ig kappa chain - h
13	454.5	69.4	129	2 S2789	Ig kappa chain v r
14	452.5	69.1	123	2 S40331	Ig kappa chain - h
15	452.5	69.1	125	2 S40333	Ig kappa chain v-j
16	451.5	68.9	108	2 S19674	Ig kappa chain v r
17	451.5	68.9	132	2 S40334	Ig kappa chain - h
18	447.5	68.3	125	2 S40316	Ig kappa chain pre
19	446	68.1	129	1 KYMS7B	Ig kappa chain v-j
20	445.5	68.0	127	2 S40367	Ig kappa chain v-i
21	444.5	67.9	108	1 K1HURY	Ig lambda chain v
22	444.5	67.9	108	2 S36277	Ig kappa chain v-i
23	441.5	67.4	108	1 K1HUBN	Ig kappa chain v-j
24	441.5	67.4	117	2 S46371	Ig kappa chain - h
25	441.5	67.4	125	2 S40350	Ig kappa chain pre
26	441	67.3	132	2 S05268	Ig kappa chain - h
27	439.5	67.1	129	2 S40369	Ig kappa chain v
28	437.5	66.8	108	2 S36279	Ig lambda chain v
29	436.5	66.6	108	1 K1HURE	Ig kappa chain v-i

30 436 66.6 106 2 PC2397 anti-tetanus toxin
31 435.5 66.5 107 2 I69017 anti-HIV envelope
32 435.5 66.5 108 1 K1HUAU Ig kappa chain v-i
33 435.5 66.5 125 2 S40353 Ig kappa chain v-j
34 434.5 66.3 110 2 S44118 Ig kappa chain v-j
35 434.5 66.3 117 2 S46376 Ig kappa chain v-j
36 434.5 66.3 123 2 S40313 Ig kappa chain v-j
37 432.5 66.0 108 1 K1HURU Ig kappa chain v-i
38 431 65.8 109 1 K1HUMV Ig kappa chain v-i
39 430.5 65.7 109 2 S31998 Ig kappa chain - h
40 430.5 65.7 129 1 K1HUDI Ig kappa chain pre
41 430 65.6 124 2 S40336 Ig kappa chain v-j
42 429.5 65.6 108 2 S44122 Ig kappa chain v r
43 429.5 65.6 131 2 S40352 Ig kappa chain v-j
44 429.5 65.6 139 2 S40365 Ig kappa chain - h
45 429.5 65.6 141 2 A49134 Ig kappa chain v-i

ALIGNMENTS

RESULT 1
A32513
Ig kappa chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
R:Accession: A32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; MUID:88331394
A:Accession: A32513
A:Molecule type: DNA
A:Residues: 1-130 <KOF>
A:Cross-references: GB:M20834; NID:g196943; PID:AAA38846.1; PID:g196944
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 76.6%; Score 502; DB 2; Length 130;
Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 MDFQVQIFSFLLISASVILSRGDIQMTQSPSLASVSGDRVTITCSATSI--TYMSWYQ 58
Db 1 MDFQVQIFSFLLISASVILSRGDIQMTQSPSLASVSGDRVTITCSATSI--TYMSWYQ 58
QY 59 QKPGKAPKLLIYDTSNLASGVPSRFGSGGTDYTLTISSLPQEDFATYTCQWSSVPLT 118
Db 61 QKPGSPKLIYDTSNLASGVPSRFGSGGTDYTLTISSLPQEDFATYTCQWSSVPLT 118
QY 119 FGGTKVEIK 128
Db 121 FGGTKLEIK 130

RESULT 2

JLO079
Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
R:Accession: JLO079; A49044; B49044
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-
A:Reference number: JLO076; MUID:89096973
A:Accession: JLO079
A:Molecule type: mRNA
A:Residues: 1-130 <KAA>
A:Cross-references: GB:M27792; NID:g197159
A:Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A>Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue

A:Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A:Title: Non-random features of the repertoire expressed by the members of one V kappa g
A:Reference number: A49044; MUID:92289826
A:Accession: A49044
A:Molecule type: DNA
A:Residues: 1-25 <ML>
A:Cross-references: GB:S37663; NID:g250214; PIDN:AA22331.1; PID:g250217
A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A:Accession: B49044
A:Molecule type: DNA
A:Residues: 114-116 <ML>
A:Cross-references: GB:S37664; NID:g250215; PIDN:AA22332.1; PID:g250218
A:Experimental source: BALB/c germ-line
A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit
A:Note: sequences extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
C:Genetics:
A:Gene: V(kappa)Ox1
A:Introns: 17/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
A:Disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match 76.0%; Score 498; DB 2; Length 235;
Best Local Similarity 74.2%; Pred. No. 7e-33;
Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60
DB 1 MDFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120
DB 61 SGTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 AGTKLEK 128

RESULT 3
S04573
A:Title: kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25058
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <FIS>
A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 498; DB 2; Length 235;
Best Local Similarity 74.2%; Pred. No. 7e-33;
Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60
DB 1 MDFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120
DB 61 SGTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 AGTKLEK 128

RESULT 5
S04573
A:Title: kappa chain precursor V region (MBL-histone 7L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: invol
A:Reference number: S04573; MUID:87133856
A:Accession: S04573
A:Molecule type: mRNA
A:Residues: 1-130 <KOF>
A:Cross-references: EMBL:X14620; NID:g52031; PIDN:CAA32773.1; PID:g52032
A:Note: the authors translated the codon AGC for residue 47 as Asn
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: heterotetramer; immunoglobulin
C:Keywords: heterotetramer; signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>

QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120
DB 61 SGTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 AGTKLEK 128

RESULT 4
PL0013
A:Title: kappa chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0013
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863
A:Accession: PL0013
A:Molecule type: mRNA
A:Residues: 1-140 <CHE>
A:Experimental source: cell line 4C11
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:46-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-118/Region: complementarity-determining 3
F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 75.0%; Score 491; DB 2; Length 140;
Best Local Similarity 74.2%; Pred. No. 1.5e-32;
Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60
DB 1 MHFQVQIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSTSSITMSYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120
DB 61 PDTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTISLQPEDFATYYCOQWSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 5
S04573
A:Title: kappa chain precursor V region (MBL-histone 7L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: invol
A:Reference number: S04573; MUID:87133856
A:Accession: S04573
A:Molecule type: mRNA
A:Residues: 1-130 <KOF>
A:Cross-references: EMBL:X14620; NID:g52031; PIDN:CAA32773.1; PID:g52032
A:Note: the authors translated the codon AGC for residue 47 as Asn
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: heterotetramer; immunoglobulin
C:Keywords: heterotetramer; signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 478; DB 2; Length 130;
Best Local Similarity 70.8%; Pred. No. 1.6e-31;
Matches 92; Conservative 22; Mismatches 14; Indels 2; Gaps 1;
QY 1 MDFQVQIFSLISASVILSRGDIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQ 58
DB 1 MDPQVQIFSLISASVILSRGDIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQ 58
QY 59 QKPGKAPKLLIYDTSNLASGVPRFSGSGGTDYTLTISLQPEDFATYYCQWSSYPLT 118
DB 61 QRSAGPKLWIYGTSLNLSGVPRFSGSGGTDYTLTISLQPEDFATYYCQWSSYPLT 118
QY 119 FGGGTKVEIK 128
DB 121 FGAGTKLEIK 130

RESULT 6
B49047
Ig kappa chain precursor V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Oct-1989 #sequence_revision 26-Oct-1989 #text_change 21-Jan-2000
C:Accession: B32456
R:Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A:Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin
A:Reference number: A32456; MUID:89174706
A:Accession: B32456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <DOM>
A:Cross-references: GB:J04610; NID:g556313; PIDN:AAA50296.1; PID:g556314
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 466; DB 2; Length 130;
Best Local Similarity 68.5%; Pred. No. 1.4e-30;
Matches 89; Conservative 21; Mismatches 18; Indels 2; Gaps 1;
QY 1 MDPVQVIFSLISASVILSRGDIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQ 58
DB 1 MDPVQVIFSLISASVILSRGDIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQ 58
QY 59 QKPGKAPKLLIYDTSNLASGVPRFSGSGGTDYTLTISLQPEDFATYYCQWSSYPLT 118
DB 61 QRSAGPKLWIYGTSLNLSGVPRFSGSGGTDYTLTISLQPEDFATYYCQWSSYPLT 118
QY 119 FGGGTKVEIK 128
DB 121 FGAGTKLEIK 130

RESULT 7
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448
A:Accession: S36264
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <GR1>
A:Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g9399919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 463.5; DB 2; Length 107;
Best Local Similarity 83.2%; Pred. No. 1.8e-30;
Matches 89; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
QY 23 DIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQKPGKAPKLLIYDTSNLASGVPS 81
DB 1 EIVLTQSPSSLSASVGDRTVITCRASQISISSYLNWYQKPGKAPKLLIYAASSLSQGVPS 60
QY 82 RFGSGSGGTDYTLTISLQPEDFATYYCQWSSYPLTFFGGGTKVEIK 128
DB 61 RFGSGSGGTDYTLTISLQPEDFATYYCQWSSYPLTFFGGGTKVEIK 107

RESULT 8
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fr
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocyt
A:Reference number: A49047; MUID:92387224
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 463.5; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 1.9e-30;
Matches 92; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 23 DIQMTQSPSSLSASVGDRTVITCSATSSIT--YMSWYQKPGKAPKLLIYDTSNLASGVPS 81
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQISISSYLNWYQKPGKAPKLLIYAASSLSQGVPS 60
QY 82 RFGSGSGGTDYTLTISLQPEDFATYYCQWSSYPLTFFGGGTKVEIK 128
DB 61 RFGSGSGGTDYTLTISLQPEDFATYYCQWSSYPLTFFGGGTKVEIK 107

RESULT 9
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

[illegible][illegible]

Job time: 162 sec

